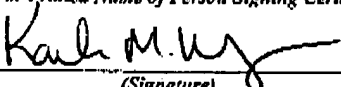


<b>CERTIFICATE OF TRANSMISSION BY FACSIMILE (37 CFR 1.8)</b>		Docket No. <b>002.00170</b>
Applicant(s): <b>Dario Alessi et al.</b>		
Application No. <b>09/937,009</b>	Filing Date <b>March 17, 2000</b>	Examiner <b>M. Monshipouri</b>
		Group Art Unit <b>1653</b>
Invention: <b>ENZYME</b>		
<p>I hereby certify that this <u>Copy of Sequence Listing as submitted on June 26, 2002 (26 pgs)</u>  <small>(Identify type of correspondence)</small></p> <p>is being facsimile transmitted to the United States Patent and Trademark Office (Fax. No. <u>571 273-0932</u>)</p> <p>on <u>Feb. 7, 2006</u>  <small>(Date)</small></p> <div style="text-align: right; margin-top: 100px;"> <u>Karla M. Weyand</u>  <small>(Typed or Printed Name of Person Signing Certificate)</small>    <small>(Signature)</small> </div>		
<p><b>Note: Each paper must have its own certificate of mailing.</b></p>		
<p><b>BEST AVAILABLE COPY</b></p>		

## SEQUENCE LISTING

<110> Alessi, Dario  
Balendran, Anudharan  
Deak, Maria  
Currie, Richard  
Downes, Peter  
Casamayor, Antonio

<120> Enzyme

<130> 002.00170

<140> US 09/937,009

<141> 2000-03-17

<150> PCT/GB00/01004

<151> 2000-03-17

<150> GB 9906245.7

<151> 1999-03-19

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 24

<212> PRT

<213> Homo sapiens

<220>

<223> region B of PRK2

<400> 1

Arg	Glu	Pro	Arg	Ile	Leu	Ser	Glu	Glu	Glu	Gln	Glu	Met	Phe	Arg	Asp
1				5				10					15		

Phe	Asp	Tyr	Ile	Ala	Asp	Trp	Cys
			20				

<210> 2

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
peptide sequence that interacts with human PRK2  
region B

<400> 2

Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Ala Arg Asp  
1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys  
20

<210> 3

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
peptide sequence that interacts with human PRK2  
region B

<400> 3

Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Phe Gly Asp  
1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys  
20

<210> 4

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<223> region A of PRK2

<400> 4

Glu Asp Val Lys Lys His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala  
1 5 10 15

Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly  
20 25 30

Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro  
35 40 45

Ile Leu Thr Pro Pro  
50

<210> 5  
<211> 23  
<212> PRT  
<213> Homo sapiens  
  
<220>  
<223> region of PKC zeta

<400> 5  
Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe  
1 5 10 15

Glu Tyr Ile Asn Pro Leu Leu  
20

<210> 6  
<211> 6  
<212> PRT  
<213> Homo sapiens  
  
<220>  
<223> portion of region B of PRK2

<400> 6  
Phe Arg Asp Phe Asp Tyr  
1 5

<210> 7  
<211> 23  
<212> PRT  
<213> Homo sapiens

<220>  
<223> region of PKC zeta

<400> 7  
Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe  
1 5 10 15

Glu Tyr Ile Asn Pro Leu Leu  
20

<210> 8  
<211> 11  
<212> PRT  
<213> Homo sapiens

<220>  
<223> region of PKB alpha

<400> 8  
Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser  
1 5 10

<210> 9  
<211> 9  
<212> PRT  
<213> Homo sapiens

<220>  
<223> region of PRK1

<400> 9  
Thr Phe Cys Gly Thr Pro Glu Phe Leu  
1 5

<210> 10  
<211> 6  
<212> PRT  
<213> Homo sapiens

<220>  
<223> region of PKC zeta

<400> 10  
Phe Glu Gly Phe Glu Tyr  
1 5

<210> 11  
<211> 13  
<212> PRT  
<213> Homo sapiens

<220>  
<223> region of PDK1

&lt;400&gt; 11

Arg Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln

1 5 10

&lt;210&gt; 12

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:pcr primer

&lt;400&gt; 12

cgggatccga ggatgtaaaa aagcacc

28

&lt;210&gt; 13

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:human PKB alpha  
substrate peptide

&lt;400&gt; 13

Arg Pro Arg Thr Ala Ala Phe

1 5

&lt;210&gt; 14

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; region of PRK2

&lt;400&gt; 14

Glu Asp Val Lys Lys His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala

1 5 10 15

Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly

20 25 30

Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro

35 40 45

5

Ile Leu Thr Pro Pro Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln  
 50 55 60

Glu Met Phe Arg Asp Phe Asp Tyr Ile Ala Asp Trp Cys  
 65 70 75

<210> 15

<211> 77

<212> PRT

<213> Homo sapiens

<220>

<223> region of PRK1

<400> 15

Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr Leu Gly Trp Glu Ala  
 1 5 10 15

Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser Gly  
 20 25 30

Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala Pro  
 35 40 45

Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu Gln  
 50 55 60

Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys  
 65 70 75

<210> 16

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<223> region of PKB alpha

<400> 16

Lys Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His  
 1 5 10 15

Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser  
 20 25 30

Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile  
 35 40 45

Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser  
 50 55 60

Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Thr Ala  
 65 70 75 80

<210> 17  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> region of P70S6k

<400> 17  
 Gly Glu Val Gln Ala His Pro Phe Phe Arg His Ile Asn Trp Glu Glu  
 1 5 10 15

Leu Leu Ala Arg Lys Val Glu Pro Pro Phe Lys Pro Leu Leu Gln Ser  
 20 25 30

Glu Glu Asp Val Ser Gln Phe Asp Ser Lys Phe Thr Arg Gln Thr Pro  
 35 40 45

Val Asp Ser Pro Asp Asp Ser Thr Leu Ser Glu Ser Ala Asn Gln Val  
 50 55 60

Phe Leu Gly Phe Thr Tyr Val Ala Pro Ser Val  
 65 70 75

<210> 18  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> region of SGK

<400> 18  
 Met Glu Ile Lys Ser His Val Phe Phe Ser Leu Ile Asn Trp Asp Asp



1                    5                    10                    15  
 Leu Ile Asn Lys Lys Ile Thr Pro Pro Phe Asn Pro Asn Val Ser Gly  
                   20                    25                    30  
 Pro Asn Glu Leu Arg His Phe Asp Pro Glu Phe Thr Glu Glu Pro Val  
                   35                    40                    45  
 Pro Asn Ser Ile Gly Lys Ser Pro Asp Ser Val Leu Val Thr Ala Ser  
                   50                    55                    60  
 Val Lys Glu Ala Ala Glu Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro  
                   65                    70                    75                    80  
 Thr Asp

<210> 19  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> region of PKC zeta

<400> 19  
 Ser Asp Ile Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu  
                   1                    5                    10                    15  
 Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp  
                   20                    25                    30  
 Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val  
                   35                    40                    45  
 Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser  
                   50                    55                    60  
 Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro Leu Leu  
                   65                    70                    75

<210> 20  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;223&gt; region of PKC alpha

&lt;400&gt; 20

Arg Asp Val Arg Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys  
1 5 10 15

Leu Glu Asn Arg Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly  
20 25 30

Lys Gly Ala Glu Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val  
35 40 45

Leu Thr Pro Pro Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp  
50 55 60

Phe Glu Gly Phe Ser Tyr Val Asn Pro Gln Phe  
65 70 75

&lt;210&gt; 21

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; region of PKA beta

&lt;400&gt; 21

Ser Asp Ile Lys Thr His Lys Trp Phe Ala Thr Thr Asp Trp Ile Ala  
1 5 10 15

Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Gly Arg  
20 25 30

Ser Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Asp Ile Arg  
35 40 45

Val Ser Ile Thr Glu Cys Ala Lys Glu Lys Phe Gly Glu Phe  
50 55 60

&lt;210&gt; 22

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> PKB consensus sequence

<220>

<223> residues 2 and 3 are variable amino acids

<400> 22

Phe Xaa Xaa Phe Ser Phe

1

5

<210> 23

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residue 6 is a variable amino acid

<400> 23

Thr Phe Cys Gly Thr Xaa Glu Leu

1

5

<210> 24

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residues 2 and 3 are variable amino acids

<220>

<223> residue 5 is serine or threonine

<220>

<223> residue 6 is phenylalanine or tyrosine

<400> 24

Phe Xaa Xaa Phe Xaa Xaa

1

5

<210> 25  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
sequence that interacts with PKB

<220>  
<223> residues 2 and 3 are variable amino acids

<220>  
<223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>  
<223> residue 5 is a negatively charged amino acid

<400> 25  
Xaa Xaa Xaa Xaa Xaa Xaa  
1 5

<210> 26  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
sequence that interacts with PKB

<220>  
<223> residues 2 and 3 are variable amino acids

<220>  
<223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>  
<223> residue 5 is aspartic acid or glutamic acid

<400> 26  
Xaa Xaa Xaa Xaa Xaa Xaa  
1 5

<210> 27  
<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
sequence that interacts with PKB

<220>

<223> residues 2 and 3 are variable amino acids

<220>

<223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>

<223> residue 5 is phospho serine or phospho threonine

<400> 27

Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 28

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residue 1 is threonine or serine

<220>

<223> residue 6 is a variable amino acid

<400> 28

Xaa Phe Cys Gly Thr Xaa Glu Leu

1

5

<210> 29

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> C terminal region of PKC zeta

&lt;400&gt; 29

Phe Glu Gly Phe Glu Tyr

1

5

&lt;210&gt; 30

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; PKB consensus sequence

&lt;220&gt;

&lt;223&gt; residues 1, 4 and 6 are phenylalanine or tyrosine

&lt;220&gt;

&lt;223&gt; residues 2 and 3 are variable amino acids

&lt;220&gt;

&lt;223&gt; residue 5 is serine or threonine

&lt;400&gt; 30

Xaa Xaa Xaa Xaa Xaa Xaa

1

5

&lt;210&gt; 31

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; PDK1 sequence

&lt;400&gt; 31

Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser

1

5

10

15

Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln

20

25

30

Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly

35

40

45

Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser

50

55

60

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu  
 65 70 75 80  
 Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val  
 85 90 95  
 Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile  
 100 105 110  
 Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr  
 115 120 125  
 Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys  
 130 135 140  
 Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser  
 145 150 155 160  
 Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser  
 165 170 175  
 Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala  
 180 185 190  
 Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro  
 195 200 205  
 Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe  
 210 215 220  
 Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn  
 225 230 235 240  
 Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu  
 245 250 255  
 Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile  
 260 265 270  
 Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr  
 275 280 285  
 Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys  
 290 295 300  
 Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp  
 305 310 315 320

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu  
325 330 335

Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln  
340 345 350

Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp  
355 360 365

Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly  
370 375 380

Cys Met Gln Val Ser Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser  
385 390 395 400

Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile  
405 410 415

His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu  
420 425 430

Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp  
435 440 445

His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp  
450 455 460

Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu  
465 470 475 480

Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly  
485 490 495

Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys  
500 505 510

Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro  
515 520 525

Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg  
530 535 540

Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln  
545 550 555

<210> 32

<211> 984



&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; PRK2 sequence

&lt;400&gt; 32

Met Ala Ser Asn Pro Glu Arg Gly Glu Ile Leu Leu Thr Glu Leu Gln  
 1 5 10 15

Gly Asp Ser Arg Ser Leu Pro Phe Ser Glu Asn Val Ser Ala Val Gln  
 20 25 30

Lys Leu Asp Phe Ser Asp Thr Met Val Gln Gln Lys Leu Asp Asp Ile  
 35 40 45

Lys Asp Arg Ile Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu  
 50 55 60

Gly Ala Glu Asn Leu Arg Lys Val Thr Thr Asp Lys Lys Ser Leu Ala  
 65 70 75 80

Tyr Val Asp Asn Ile Leu Lys Lys Ser Asn Lys Lys Leu Glu Glu Leu  
 85 90 95

His His Lys Leu Gln Glu Leu Asn Ala His Ile Val Val Ser Asp Pro  
 100 105 110

Glu Asp Ile Thr Asp Cys Pro Arg Thr Pro Asp Thr Pro Asn Asn Asp  
 115 120 125

Pro Arg Cys Ser Thr Ser Asn Asn Arg Leu Lys Ala Leu Gln Lys Gln  
 130 135 140

Leu Asp Ile Glu Leu Lys Val Lys Gln Gly Ala Glu Asn Met Ile Gln  
 145 150 155 160

Met Tyr Ser Asn Gly Ser Ser Lys Asp Arg Lys Leu His Gly Thr Ala  
 165 170 175

Gln Gln Leu Leu Gln Asp Ser Lys Thr Lys Ile Glu Val Ile Arg Met  
 180 185 190

Gln Ile Leu Gln Ala Val Gln Thr Asn Glu Leu Ala Phe Asp Asn Ala  
 195 200 205

Lys Pro Val Ile Ser Pro Leu Glu Leu Arg Met Glu Glu Leu Arg His  
 210 215 220

His Phe Arg Ile Glu Phe Ala Val Ala Glu Gly Ala Lys Asn Val Met  
 225 230 235 240  
 Lys Leu Leu Gly Ser Gly Lys Val Thr Asp Arg Lys Ala Leu Ser Glu  
 245 250 255  
 Ala Gln Ala Arg Phe Asn Glu Ser Ser Gln Lys Leu Asp Leu Leu Lys  
 260 265 270  
 Tyr Ser Leu Glu Gln Arg Leu Asn Glu Val Pro Lys Asn His Pro Lys  
 275 280 285  
 Ser Arg Ile Ile Ile Glu Glu Leu Ser Leu Val Ala Ala Ser Pro Thr  
 290 295 300  
 Leu Ser Pro Arg Gln Ser Met Ile Ser Thr Gln Asn Gln Tyr Ser Thr  
 305 310 315 320  
 Leu Ser Lys Pro Ala Ala Leu Thr Gly Thr Leu Glu Val Arg Leu Met  
 325 330 335  
 Gly Cys Gln Asp Ile Leu Glu Asn Val Pro Gly Arg Ser Lys Ala Thr  
 340 345 350  
 Ser Val Ala Leu Pro Gly Trp Ser Pro Ser Glu Thr Arg Ser Ser Phe  
 355 360 365  
 Met Ser Arg Thr Ser Lys Ser Lys Ser Gly Ser Ser Arg Asn Leu Leu  
 370 375 380  
 Lys Thr Asp Asp Leu Ser Asn Asp Val Cys Ala Val Leu Lys Leu Asp  
 385 390 395 400  
 Asn Thr Val Val Gly Gln Thr Ser Trp Lys Pro Ile Ser Asn Gln Ser  
 405 410 415  
 Trp Asp Gln Lys Phe Thr Leu Glu Leu Asp Arg Ser Arg Glu Leu Glu  
 420 425 430  
 Ile Ser Val Tyr Trp Arg Asp Trp Arg Ser Leu Cys Ala Val Lys Phe  
 435 440 445  
 Leu Arg Leu Glu Asp Phe Leu Asp Asn Gln Arg His Gly Met Cys Leu  
 450 455 460  
 Tyr Leu Glu Pro Gln Gly Thr Leu Phe Ala Glu Val Thr Phe Phe Asn  
 465 470 475 480

Pro Val Ile Glu Arg Arg Pro Lys Leu Gln Arg Gln Lys Lys Ile Phe  
 485 490 495

Ser Lys Gln Gln Gly Lys Thr Phe Leu Arg Ala Pro Gln Met Asn Ile  
 500 505 510

Asn Ile Ala Thr Trp Gly Arg Leu Val Arg Arg Ala Ile Pro Thr Val  
 515 520 525

Asn His Ser Gly Thr Phe Ser Pro Gln Ala Pro Val Pro Thr Thr Val  
 530 535 540

Pro Val Val Asp Val Arg Ile Pro Gln Leu Ala Pro Pro Ala Ser Asp  
 545 550 555 560

Ser Thr Val Thr Lys Leu Asp Phe Asp Leu Glu Pro Glu Pro Pro Pro  
 565 570 575

Ala Pro Pro Arg Ala Ser Ser Leu Gly Glu Ile Asp Glu Ser Ser Glu  
 580 585 590

Leu Arg Val Leu Asp Ile Pro Gly Gln Asp Ser Glu Thr Val Phe Asp  
 595 600 605

Ile Gln Asn Asp Arg Asn Ser Ile Leu Pro Lys Ser Gln Ser Glu Tyr  
 610 615 620

Lys Pro Asp Thr Pro Gln Ser Gly Leu Glu Tyr Ser Gly Ile Gln Glu  
 625 630 635 640

Leu Glu Asp Arg Arg Ser Gln Gln Arg Phe Gln Phe Asn Leu Gln Asp  
 645 650 655

Phe Arg Cys Cys Ala Val Leu Gly Arg Gly His Phe Gly Lys Val Leu  
 660 665 670

Leu Ala Glu Tyr Lys Asn Thr Asn Glu Met Phe Ala Ile Lys Ala Leu  
 675 680 685

Lys Lys Gly Asp Ile Val Ala Arg Asp Glu Val Asp Ser Leu Met Cys  
 690 695 700

Glu Lys Arg Ile Phe Glu Thr Val Asn Ser Val Arg His Pro Phe Leu  
 705 710 715 720

Val Asn Leu Phe Ala Cys Phe Gln Thr Lys Glu His Val Cys Phe Val  
 725 730 735

Met Glu Tyr Ala Ala Gly Gly Asp Leu Met Met His Ile His Thr Asp  
740 745 750

Val Phe Ser Glu Pro Arg Ala Val Phe Tyr Ala Ala Cys Val Val Leu  
755 760 765

Gly Leu Gln Tyr Leu His Glu His Lys Ile Val Tyr Arg Asp Leu Lys  
770 775 780

Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly Phe Val Lys Ile Ala Asp  
785 790 795 800

Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr Gly Asp Arg Thr Ser Thr  
805 810 815

Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro Glu Val Leu Thr Glu Thr  
820 825 830

Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly Leu Gly Val Leu Ile Tyr  
835 840 845

Glu Met Leu Val Gly Glu Ser Pro Phe Pro Gly Asp Asp Glu Glu Glu  
850 855 860

Val Phe Asp Ser Ile Val Asn Asp Glu Val Arg Tyr Pro Arg Phe Leu  
865 870 875 880

Ser Thr Glu Ala Ile Ser Ile Met Arg Arg Leu Leu Arg Arg Asn Pro  
885 890 895

Glu Arg Arg Leu Gly Ala Ser Glu Lys Asp Ala Glu Asp Val Lys Lys  
900 905 910

His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala Leu Met Asp Lys Lys  
915 920 925

Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly Arg Glu Asp Val Ser  
930 935 940

Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro Ile Leu Thr Pro Pro  
945 950 955 960

Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Phe Arg Asp  
965 970 975

Phe Asp Tyr Ile Ala Asp Trp Cys  
980

<210> 33  
 <211> 942  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> PRK1 sequence

<400> 33  
 Met Ala Ser Asp Ala Val Gln Ser Glu Pro Arg Ser Trp Ser Leu Leu  
 1 5 10 15  
 Glu Gln Leu Gly Leu Ala Gly Ala Asp Leu Ala Ala Pro Gly Val Gln  
 20 25 30  
 Gln Gln Leu Glu Leu Glu Arg Glu Arg Leu Arg Arg Glu Ile Arg Lys  
 35 40 45  
 Glu Leu Lys Leu Lys Glu Gly Ala Glu Asn Leu Arg Arg Ala Thr Thr  
 50 55 60  
 Asp Leu Gly Arg Ser Leu Gly Pro Val Glu Leu Leu Leu Arg Gly Ser  
 65 70 75 80  
 Ser Arg Arg Leu Asp Leu Leu His Gln Gln Leu Gln Glu Leu His Ala  
 85 90 95  
 His Val Val Leu Pro Asp Pro Ala Ala Thr His Asp Gly Pro Gln Ser  
 100 105 110  
 Pro Gly Ala Gly Gly Pro Thr Cys Ser Ala Thr Asn Leu Ser Arg Val  
 115 120 125  
 Ala Gly Leu Glu Lys Gln Leu Ala Ile Glu Leu Lys Val Lys Gln Gly  
 130 135 140  
 Ala Glu Asn Met Ile Gln Thr Tyr Ser Asn Gly Ser Thr Lys Asp Arg  
 145 150 155 160  
 Lys Leu Leu Leu Thr Ala Gln Gln Met Leu Gln Asp Ser Lys Thr Lys  
 165 170 175  
 Ile Asp Ile Ile Arg Met Gln Leu Arg Arg Ala Leu Gln Ala Asp Gln  
 180 185 190  
 Leu Glu Asn Gln Ala Ala Pro Asp Asp Thr Gln Gly Ser Pro Asp Leu

195	200	205
Gly Ala Val Glu Leu Arg	Ile Glu Glu Leu Arg	His His Phe Arg Val
210	215	220
Glu His Ala Val Ala Glu Gly Ala Lys Asn Val Leu Arg Leu Leu Ser		
225	230	235 240
Ala Ala Lys Ala Pro Asp Arg Lys Ala Val Ser Glu Ala Gln Glu Lys		
245	250	255
Leu Thr Glu Ser Asn Gln Lys Leu Gly Leu Leu Arg Glu Ala Leu Glu		
260	265	270
Arg Arg Leu Gly Glu Leu Pro Ala Asp His Pro Lys Gly Arg Leu Leu		
275	280	285
Arg Glu Glu Leu Ala Ala Ala Ser Ser Ala Ala Phe Ser Thr Arg Leu		
290	295	300
Ala Gly Pro Phe Pro Ala Thr His Tyr Ser Thr Leu Cys Lys Pro Ala		
305	310	315 320
Pro Leu Thr Gly Thr Leu Glu Val Arg Val Val Gly Cys Arg Asp Leu		
325	330	335
Pro Glu Thr Ile Pro Trp Asn Pro Thr Pro Ser Met Gly Gly Pro Gly		
340	345	350
Thr Pro Asp Ser Arg Pro Pro Phe Leu Ser Arg Pro Ala Arg Gly Leu		
355	360	365
Tyr Ser Arg Ser Gly Ser Leu Ser Gly Arg Ser Ser Leu Lys Ala Glu		
370	375	380
Ala Glu Asn Thr Ser Glu Val Ser Thr Val Leu Lys Leu Asp Asn Thr		
385	390	395 400
Val Val Gly Gln Thr Ser Trp Lys Pro Cys Gly Pro Asn Ala Trp Asp		
405	410	415
Gln Ser Phe Thr Leu Glu Leu Glu Arg Ala Arg Glu Leu Glu Leu Ala		
420	425	430
Val Phe Trp Arg Asp Gln Arg Gly Leu Cys Ala Leu Lys Phe Leu Lys		
435	440	445
Leu Glu Asp Phe Leu Asp Asn Glu Arg His Glu Val Gln Leu Asp Met		

450                      455                      460  
 Glu Pro Gln Gly Cys Leu Val Ala Glu Val Thr Phe Arg Asn Pro Val  
 465                      470                      475                      480  
 Ile Glu Arg Ile Pro Arg Leu Arg Arg Gln Lys Lys Ile Phe Ser Lys  
                     485                      490                      495  
 Gln Gln Gly Lys Ala Phe Gln Arg Ala Arg Gln Met Asn Ile Asp Val  
                     500                      505                      510  
 Ala Thr Trp Val Arg Leu Leu Arg Arg Leu Ile Pro Asn Ala Thr Gly  
                     515                      520                      525  
 Thr Gly Thr Phe Ser Pro Gly Ala Ser Pro Gly Ser Glu Ala Arg Thr  
                     530                      535                      540  
 Thr Gly Asp Ile Ser Val Glu Lys Leu Asn Leu Gly Thr Asp Ser Asp  
 545                      550                      555                      560  
 Ser Ser Pro Gln Lys Ser Ser Arg Asp Pro Pro Ser Ser Pro Ser Ser  
                     565                      570                      575  
 Leu Ser Ser Pro Ile Gln Glu Ser Thr Ala Pro Glu Leu Pro Ser Glu  
                     580                      585                      590  
 Thr Gln Glu Thr Pro Gly Pro Ala Leu Cys Ser Pro Leu Arg Lys Ser  
                     595                      600                      605  
 Pro Leu Thr Leu Glu Asp Phe Lys Phe Leu Ala Val Leu Gly Arg Gly  
                     610                      615                      620  
 His Phe Gly Lys Val Leu Leu Ser Glu Phe Arg Pro Ser Gly Glu Leu  
 625                      630                      635                      640  
 Phe Ala Ile Lys Ala Leu Lys Lys Gly Asp Ile Val Ala Arg Asp Glu  
                     645                      650                      655  
 Val Glu Ser Leu Met Cys Glu Lys Arg Ile Leu Ala Ala Val Thr Ser  
                     660                      665                      670  
 Ala Gly His Pro Phe Leu Val Asn Leu Phe Gly Cys Phe Gln Thr Pro  
                     675                      680                      685  
 Glu His Val Cys Phe Val Met Glu Tyr Ser Ala Gly Gly Asp Leu Met  
                     690                      695                      700  
 Leu His Ile His Ser Asp Val Phe Ser Glu Pro Arg Ala Ile Phe Tyr

```

705              710              715              720
Ser Ala Cys Val Val Leu Gly Leu Gln Phe Leu His Glu His Lys Ile
              725              730              735
Val Tyr Arg Asp Leu Lys Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly
              740              745              750
Tyr Val Lys Ile Ala Asp Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr
              755              760              765
Gly Asp Arg Thr Ser Thr Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro
              770              775              780
Glu Val Leu Thr Asp Thr Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly
785              790              795              800
Leu Gly Val Leu Leu Tyr Glu Met Leu Val Gly Glu Ser Pro Phe Pro
              805              810              815
Gly Asp Asp Glu Glu Glu Val Phe Asp Ser Ile Val Asn Asp Glu Val
              820              825              830
Arg Tyr Pro Arg Phe Leu Ser Ala Glu Ala Ile Gly Ile Met Arg Arg
              835              840              845
Leu Leu Arg Arg Asn Pro Glu Arg Arg Leu Gly Ser Ser Glu Arg Asp
              850              855              860
Ala Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr Leu Gly Trp Glu
865              870              875              880
Ala Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser
              885              890              895
Gly Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala
              900              905              910
Pro Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu
              915              920              925
Gln Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys
              930              935              940

```

<210> 34  
 <211> 592  
 <212> PRT



&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; PKC zeta sequence

&lt;400&gt; 34

Met Pro Ser Arg Thr Asp Pro Lys Met Glu Gly Ser Gly Gly Arg Val  
 1 5 10 15

Arg Leu Lys Ala His Tyr Gly Gly Asp Ile Phe Ile Thr Ser Val Asp  
 20 25 30

Ala Ala Thr Thr Phe Glu Glu Leu Cys Glu Glu Val Arg Asp Met Cys  
 35 40 45

Arg Leu His Gln Gln His Pro Leu Thr Leu Lys Trp Val Asp Ser Glu  
 50 55 60

Gly Asp Pro Cys Thr Val Ser Ser Gln Met Glu Leu Glu Glu Ala Phe  
 65 70 75 80

Arg Leu Ala Arg Gln Cys Arg Asp Glu Gly Leu Ile Ile His Val Phe  
 85 90 95

Pro Ser Thr Pro Glu Gln Pro Gly Leu Pro Cys Pro Gly Glu Asp Lys  
 100 105 110

Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu Tyr Arg Ala  
 115 120 125

Asn Gly His Leu Phe Gln Ala Lys Arg Phe Asn Arg Arg Ala Tyr Cys  
 130 135 140

Gly Gln Cys Ser Glu Arg Ile Trp Gly Leu Ala Arg Gln Gly Tyr Arg  
 145 150 155 160

Cys Ile Asn Cys Lys Leu Leu Val His Lys Arg Cys His Gly Leu Val  
 165 170 175

Pro Leu Thr Cys Arg Lys His Met Asp Ser Val Met Pro Ser Gln Glu  
 180 185 190

Pro Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu  
 195 200 205

Thr Asp Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Ser Ile  
 210 215 220

Lys Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly  
 225 230 235 240  
 Ile Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg  
 245 250 255  
 Val Ile Gly Arg Gly Thr Tyr Ala Lys Val Leu Leu Val Arg Leu Lys  
 260 265 270  
 Lys Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val  
 275 280 285  
 His Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe  
 290 295 300  
 Glu Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe  
 305 310 315 320  
 Gln Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly  
 325 330 335  
 Asp Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His  
 340 345 350  
 Ala Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His  
 355 360 365  
 Glu Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu  
 370 375 380  
 Asp Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu  
 385 390 395 400  
 Gly Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn  
 405 410 415  
 Tyr Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val  
 420 425 430  
 Asp Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg  
 435 440 445  
 Ser Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp  
 450 455 460  
 Tyr Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe  
 465 470 475 480

Leu Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp  
485 490 495

Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile  
500 505 510

Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys  
515 520 525

Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly  
530 535 540

Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr  
545 550 555 560

Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu  
565 570 575

Gly Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val  
580 585 590

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.